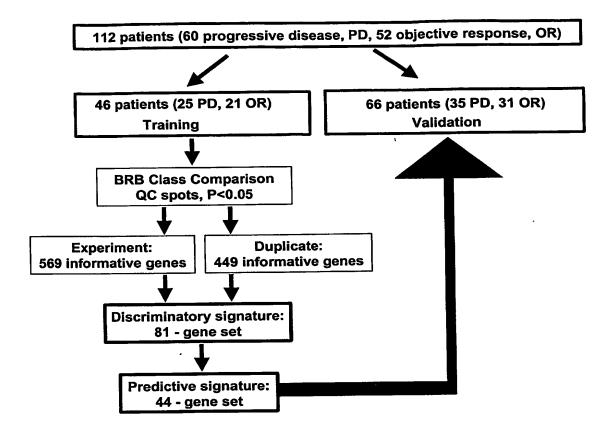
WO 2005/054510 PCT/IB2004/004405

Figure 1



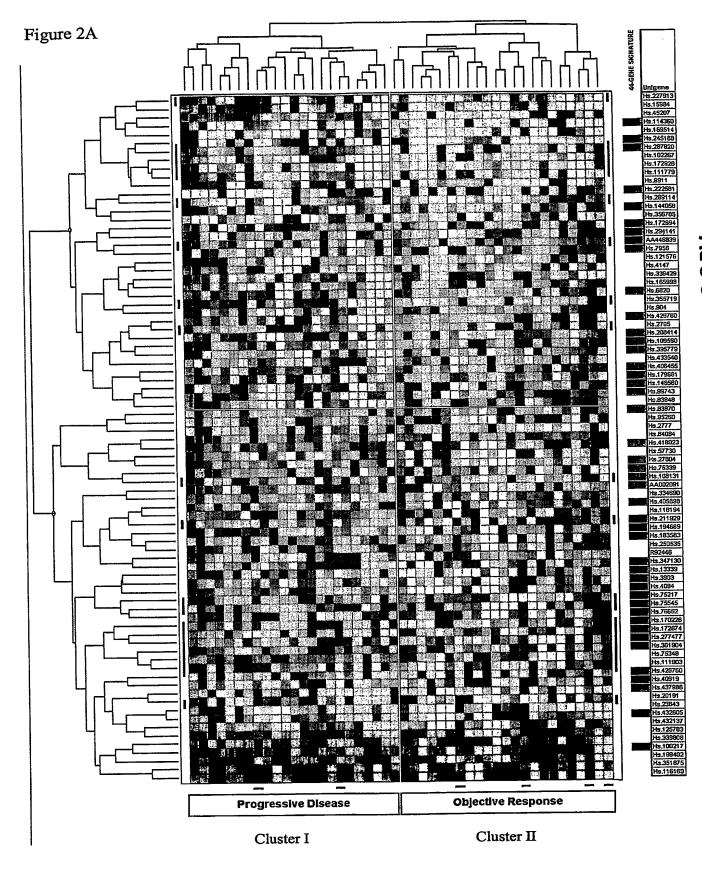


Figure 2B

. 1					
The state of the s					
			l l		
:					
1			ł		
1					ER regulation
	Unigene	Gene_Symbol		SWISSPROT Keywords	EKTERMERON
	Hs.227913	APi5	11p12-q12		
ľ	Hs.15984	LOC51186	Xq22.1		- 8
	Hs.45207	CHDS-pending	20112		
	Hs.114360	TSC22	13014	Franscription regulation; Repressor, Nuclear protein.	21
	Hs.169514				
	Hs.245188	TMP3		deta improtesse tributor.	19
Ė	Hs.287620	FNI	2q34	Cell adhesion.	
	Hs.102267	LOX	5q23.2		
	Hs.172928	COL1A1	17q21.3-q22.1	Extracelutar matrix.	
	Hs.111779	SPARC	5q31.3-q32	Extracellular matrix.	17
	Hs.8911	FLJ11773	12q13.13		
	Hs.222581				
_	Hs.289114	TNC	9q33	ExtraceCular matric Cell cohesion.	
	Hs.144058		17q25.2		
	Hs.358788	GNAQ	9q21.2		
	Hs.172694		17q12		i
-	Hs 294141	SMARCA4	19013.3		
=	AA445B39		10q26.3		
f	Hs.7956	 	<u>-</u>		
	Hs.121576	MY01B	2012-034	Myosin, ATP-binding, Actin-binding, Calmoduch-binding.	
	Hs.4147	TRAM	Bq13.1	Endoplosmic reliculum, Transmembrane, Glycoprotein.	
	Hs.336429		12p13.31		17
	Hs.165998		1p31-p22		
	Hs.6820	CFPI	10p11.21		8
-	Hs.355719		5q35	Nuclear protein; Phosphoryletion; RNA-binding; Proto-oncogene.	L
	Hs.904	AGL	1p21	Glycogen biosynthesis; Glycosyltransferese.	
	Hs.429780		1 -		
-	Hs.2795	LDHA	11p15.4	Oxidoreduciase; NAD; Glycolysis.	20
	Hs.208414		1,0,0,0,0		
_	Hs.109590		4q24-q25		
			1p35.23		1
_	Hs.395779		1p35.2	Chaperone.	
	Hs.433540		10q21-q22	Glycoprotein; Lysosome; Sphingolipid metabolism.	
	Hs.40645		6p21.33	Microtubule: GTP-binding.	
	Hs.179661			Lyase; Glycolysis; Magnesium.	17
_	Hs.146581	ENO2	12p13	Lyase, Olycarysis, magnitosiani.	18
	Hs.89743		40-40	Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis.	-
	Hs.8384B	TPII	12p13		
i, a s	Hs.83870		2022	Actin-binding, Muscle protein, Cytoskeleton.	
	Hs.85260		6p22-p23	Serine protesse inhibitor.	-
	Hs.2777	ITH	3p21.2-p21.1	Serine processe unutur.	
	Hs.84084	APPBP2	17q21-q23		-
	Hs.41802			I	-
	Hs.57730		1q42.13	Hypothetical protein; Transmembrane.	
	Hs.27804				-
	Hs.75339		11q23	In the Table Assess Constants	
_,	Hs.10813		7q34-q35	Hydrolase, Thiol protease, Apoptosis.	
	AA00209		5q14.1		-
_	Hs.33469				-
į.	Hs.40589		11q23.3		-
_	Hs.11819		3922.3		
	Hs.21192		22q13.1	Redox-active center, Electron transport, Machondrian.	- <u>-</u> -
	Hs.19466		17q21.1-q21.3		-
	Hs.18358		6p25	Serpin, Serine protease inhibitor.	-
	Hs.25053	5 RABSEP	17p13.2		
	R92446				-[
	Hs.34713		19p13.11		_
	Hs.13339		17p11.2-p12		-1
ï	Hs.3903	CDC42EP4	17q24-q25	Cytoskeleton.	21
	Hs.4084	KIAA1025	12q24.22		-
Ī	Hs.75217	MAP2K4	17p11.2	Serine/threonine-protein kinase; Tyrosine-protein kinase.	_
Ī	Hs.75545			Receptor; Transmembrane; Glycoprotein.	-
ī	Hs.76662		10q24.1		_
	Hs.1702		9q33.1		_
	Hs.1726		16q22.2	Transcription regulation, Activator, Nuclear protein, DNA-binding.	_
	Hs.2774		6p21.3	MHC t, Transmembrane; Glycoprotein.	18
F	Hs,3018		1q21.3		_
	Hs.75340		14q11.2	Proteasome; Interferon Induction.	8
	Hs.1119		18q13.3	IgO-binding protein; Receptor, Transmembrane; Glycoprotein.	
	Hs.4287		-		
	Hs.4091		9922.33		
				-	8
	Hs.4379		2~25	-	8
	Hs.2019		3q25 Xq28.1	-	
	Hs 2364			Glycosytransierose, Endoplasmic refloutum.	17
	Hs.4326		9:31 -	Out-costmanous coof mandagenes township	
	H3.4321				
	Hs.1257		1p32.3		
	Hs.3398		17q21.31		6
		17 FMNL	17q21		-
	Hs.1002		20-11-01		
	Hs.1002 Hs.1994 Hs.3518	02 LFD1L	22q11.21 8q22-q23	Ubi conjugation pathway. Oxidoreductasse; Inner membrane; Milechandrian.	

Figure 3

